STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/525,324_

Source: _Pct/10_

Date Processed by STIC: _3/4/05_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.2.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
   http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
   U.S. Patent and Trademark Office. Mail Stop Sequence, Customer Window, Randolph Building. 401 Dulany Street. Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/525,324

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics / Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

·2 ____ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ____ Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length — Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 ____ Skipped Sequences (OLD RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences (NEW RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____ Invalid <213> Response — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ____ Use of <220> — Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n/Xaa — "n" can only represent a single <u>nucleotide</u>; "Xaa" can only represent a single <u>amino acid</u>

PCT

RAW SEQUENCE LISTING   DATE: 03/04/2005
PATENT APPLICATION: US/10/525,324   TIME: 12:18:01

    Input Set : A:\PTO.FG.txt   *see item 4 on Error*
    Output Set: N:\CRF4\03042005\J525324.raw   *Summary Sheet*

   4 <110> APPLICANT: KYOWA HAKKO KOGYO CO., LTD
   6 <120> TITLE OF INVENTION: An agent for prevention and/or treatment of itching
   8 <130> FILE REFERENCE: 11503WO1
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/525,324
C--> 11 <141> CURRENT FILING DATE: 2005-02-22
  13 <150> PRIOR APPLICATION NUMBER: JP 2002/241522
  14 <151> PRIOR FILING DATE: 2002-08-22
  16 <160> NUMBER OF SEQ ID NOS: 20
  18 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES   *Does Not Comply*
                                           Corrected Diskette Needed

   525 <210> SEQ ID NO: 15
   526 <211> LENGTH: (36) *34 shown below*
   527 <212> TYPE: DNA
   528 <213> ORGANISM: Artificial Sequence
W--> 529 <220> FEATURE:
   530 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic DNA
   532 <400> SEQUENCE: 15   *insert a space after each*
E--> 533 ataagcttgccaccatggacaacagcacgggcac   *group of (36) 34*
   536 <210> SEQ ID NO: 16
   537 <211> LENGTH: (33) 31   *10 nucleotides*
   538 <212> TYPE: DNA
   539 <213> ORGANISM: Artificial Sequence
W--> 540 <220> FEATURE:
   541 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic DNA
   543 <400> SEQUENCE: 16   *insert a space*
E--> 544 tagcggccgctcactgtgccgggggcagcag   (33) 31
   733 <210> SEQ ID NO: 20
   734 <211> LENGTH: 19
   735 <212> TYPE: DNA
   736 <213> ORGANISM: Artificial Sequence
   738 <220> FEATURE:
   739 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic DNA
   741 <400> SEQUENCE: 20 *insert a space*
   742 cattggccatctcctgggg   19
E--> 746 (1/21) *delete*

Please insert a space after each
group of 10 nucleotides
in Sequence 19, too

VERIFICATION SUMMARY   DATE: 03/04/2005
PATENT APPLICATION: **US/10/525,324**   TIME: 12:18:02

Input Set : **A:\PTO.FG.txt**
Output Set: **N:\CRF4\03042005\J525324.raw**

L:10 M:270 C: Current Application Number differs, Replaced Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:529 M:283 W: Missing Blank Line separator, <220> field identifier
L:533 M:254 E: No. of Bases conflict, LENGTH:Input:36 Counted:34 SEQ:15
L:533 M:252 E: No. of Seq. differs, <211> LENGTH:Input:36 Found:34 SEQ:15
L:540 M:283 W: Missing Blank Line separator, <220> field identifier
L:544 M:254 E: No. of Bases conflict, LENGTH:Input:33 Counted:31 SEQ:16
L:544 M:252 E: No. of Seq. differs, <211> LENGTH:Input:33 Found:31 SEQ:16
L:746 M:254 E: No. of Bases conflict, LENGTH:Input:21 Counted:20 SEQ:20
L:746 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:746 M:252 E: No. of Seq. differs, <211> LENGTH:Input:19 Found:20 SEQ:20